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DB=USPT; PLUR=YES; OP=AND

L1 (atp-g or atpg or f1f0 or f0f1 or fofi).clm.

17 L1

DB=JPAB,EPAB,DWPI; PLUR=YES; OP=AND

L2 (atp-g or atpg or f1f0 or f0f1 or fofi).clm.

0 L2

DB=USPT; PLUR=YES; OP=AND

L3 atp\$.clm.

766 L3

DB=JPAB,EPAB,DWPI; PLUR=YES; OP=AND

L4 atp\$.clm.

0 L4

L3 and (mutant or mutation or mutagenesis

L5 * or recombinant or altered or alteration of
insertion or substitution or deletion).clm.

0 L5

DB=USPT; PLUR=YES; OP=AND

L3 and (mutant or mutation or mutagenesis

L6 or recombinant or altered or alteration of
insertion or substitution or deletion).clm.

90 L6

L7 L6 and gamma

36 L7

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SWISS-PROT: 001666

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ID ATPG_DROME STANDARD; PRT; 297 AA.
AC 001666; Q9VAH8;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14).
GN ATPSYN-GAMMA OR CG7610.
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132; [NCBI, ExpASY, EBI, Israel, Japan]
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195 (2000).
 RN [2]
 RP SEQUENCE OF 1-169 FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=99168769; PubMed=10071211; [NCBI, ExPASy, EBI, Israel, Japan]
 RA Caggese C., Ragone G., Perrini B., Moschetti R., De Pinto V.,
 RA Caizzi R., Barsanti P.;
 RT "Identification of nuclear genes encoding mitochondrial proteins:
 RT isolation of a collection of *D. melanogaster* cDNAs homologous to
 RT sequences in the Human Gene Index database.";
 RL Mol. Gen. Genet. 261:64-70 (1999).
 CC -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
 CC GRADIENT ACROSS THE MEMBRANE. THE GAMMA CHAIN IS BELIEVED TO BE
 CC IMPORTANT IN REGULATING ATPASE ACTIVITY AND THE FLOW OF PROTONS
 CC THROUGH THE CF(0) COMPLEX.
 CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
 CC H(+) (Out).
 CC -!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
 CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
 CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
 CC HAS THREE MAIN SUBUNITS: A, B AND C.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.
 CC -!- SIMILARITY: BELONGS TO THE ATPASE GAMMA CHAIN FAMILY.
 CC -----
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 CC -----
 DR EMBL; AE003771; AAF56932.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
 DR EMBL; Y12701; CAA73233.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
 DR FlyBase; FBgn0020235; ATPsyn-gamma.
 DR InterPro; IPR000131; ATPase gamma.
 DR InterPro; Graphical view of domain structure.
 DR Pfam; PF00231; ATP-synt; 1.
 DR PRINTS; PR00126; ATPASEGAMMA.
 DR TIGRFAMS; TIGR01146; ATPsyn Flgamma; 1.
 DR PROSITE; PS00153; ATPASE GAMMA; 1.
 DR ProDom [Domain structure / List of seq. sharing at least 1 domain]
 DR BLOCKS; O01666.
 DR ProtoNet; O01666.
 DR ProtoMap; O01666.
 DR PRESAGE; O01666.
 DR DIP; O01666.
 DR ModBase; O01666.
 DR SWISS-2DPAGE; GET REGION ON 2D PAGE.
 KW ATP synthesis; CF(1); Hydrogen ion transport; Hydrolase;
 KW Mitochondrion; Transit peptide.
 FT TRANSIT 1 ? MITOCHONDRION (POTENTIAL).
 FT CHAIN ? 297 ATP SYNTHASE GAMMA CHAIN.
 SQ SEQUENCE 297 AA; 32871 MW; B648B8D614E01FCE CRC64;
 MMMQRTQLLL PLAMEATMLA QQQRGMATLK MISIRLKSVK NIKKITQSMK MVSAKYARA
 ERDLKAARPY GIGAQQFFEK TEIQPDEKAE PKLLIAVTS DRGLCGAVHT GVARLIRGEL
 AQDEANTKVF CVGDKSRail SRLYGKNILM VANEVGR LPP TFLDASKIAN EVLQTGYDYT
 EGKIVYNRFK SVVSYQCSTL PIFSGSTVEK SEKLAVYDSL DSDVVKSYLE FSLASLIFYT

MKEGACSEQS SRMTAMDNAS KNAGEMIDKL TLTFNRTRQA VITRELIEII SGAAALT

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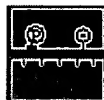


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Sequence analysis tools:

[ProtParam](#), [ProtScale](#),
[Compute pI/Mw](#), [PeptideMass](#),
[PeptideCutter](#), [Dotlet](#) (Java)



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[SWALL \(SPTR\)](#)[Save](#)[Link](#)[Launch](#)[BlastP](#)[Printer Friendly](#)[General](#) [Description](#) [References](#) [Comments](#) [Links](#) [Keywords](#) [Seq](#)**General information****Entry name** ATPG_ECOLI**Accession number** [P00837](#), [P00838](#)**Created** Rel. 01, 21-JUL-1986**Sequence update** Rel. 01, 21-JUL-1986**Annotation update** Rel. 41, 15-JUN-2002**Description and origin of the Protein****Description** ATP synthase gamma chain (EC [3.6.3.14](#)).**Gene name(s)** ATPG OR UNCG OR PAPC OR B3733 OR Z5231 OR**Organism source** Escherichia coli
Escherichia coli O157:H7.**Taxonomy** Bacteria; Proteobacteria; gamma subdivision; Enterobact**NCBI TaxID** [562](#), [83334](#)**References**

- [1] Walker,J.E., Gay,N.J., Saraste,M., Eberle,A.N.,
**DNA sequence around the Escherichia coli unc opero
sequence of a 17 kilobase segment containing asnA, o
phoS.**

(1984) *Biochem. J.* **224**:799-815

Position	SEQUENCE FROM N.A.
----------	--------------------

Medline	85121806
---------	--------------------------

PubMed	6395859
--------	-------------------------

- [2] Saraste,M., Gay,N.J., Eberle,A., Runswick,M.J., Walker
**The atp operon: nucleotide sequence of the genes for
epsilon subunits of Escherichia coli ATP synthase.**
(1981) *Nucleic Acids Res.* **9**:5287-5296

Position	SEQUENCE FROM N.A.
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Medline	82059507
---------	--------------------------

PubMed	6272217
--------	-------------------------

- [3] Kanazawa,H., Kayano,T., Mabuchi,K., Futai,M.,

		Nucleotide sequence of the genes coding for alpha, beta subunits of the proton-translocating ATPase of Escherichia coli (1981) <i>Biochem. Biophys. Res. Commun.</i> 103 :604-612	
		Position	SEQUENCE FROM N.A.
		Medline	<u>82134798</u>
		PubMed	<u>6277310</u>
[4]		Burland, V.D., Plunkett, G. III, Daniels, D.L., Blattner, F.R. DNA sequence and analysis of 136 kilobases of the Escherichia coli genome: organizational symmetry around the origin of replication (1993) <i>Genomics</i> 16 :551-561	
		Position	SEQUENCE FROM N.A.
		Comments	STRAIN=K12 / MG1655;
		Medline	<u>93315143</u>
[5]		Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Fink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Dimalanta, E.T., Potamou, K., Apodaca, J., Anantharaman, G., Schwartz, D.C., Welch, R.A., Blattner, F.R., Genome sequence of enterohaemorrhagic Escherichia coli O157:H7 (2001) <i>Nature</i> 409 :529-533	
		Position	SEQUENCE FROM N.A.
		Comments	STRAIN=O157:H7 / EDL933 / A
		Medline	<u>21074935</u>
[6]		Hayashi, T., Makino, K., Ohnishi, M., Kurokawa, K., Ishii, H., Han, C.-G., Ohtsubo, E., Nakayama, K., Murata, T., Tanaka, H., Honda, T., Sasakawa, C., Ogasawara, N., Yasu, S., Shiba, T., Hattori, M., Shinagawa, H., Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain (2001) <i>DNA Res.</i> 8 :11-22	
		Position	SEQUENCE FROM N.A.
		Comments	STRAIN=O157:H7 / RIMD 0509
		Medline	<u>21156231</u>
[7]		Iwamoto, A., Miki, J., Maeda, M., Futai, M., H(+)-ATPase gamma subunit of Escherichia coli. Role of the carboxyl-terminal region. (1990) <i>J. Biol. Chem.</i> 265 :5043-5048	
		Position	SEQUENCE OF 261-287 FROM

	Medline	<u>90202983</u>
	PubMed	<u>2138624</u>
[8]	Hausrath,A.C., Grueber,G., Matthews,B.W., Capaldi,R. Structural features of the gamma subunit of the Esch ATPase revealed by a 4.4-A resolution map obtained crystallography. (1999) <i>Proc. Natl. Acad. Sci. U.S.A.</i> 96 :13697-13702	
	Position	X-RAY CRYSTALLOGRAPHY
	Medline	<u>20040613</u>
	PubMed	<u>10570135</u>

Comments

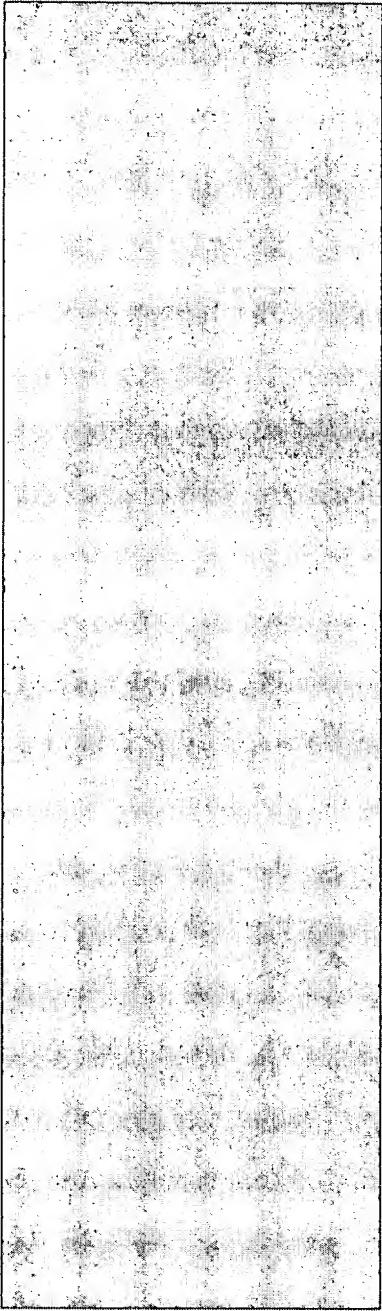
FUNCTION	PRODUCES ATP FROM ADP I OF A PROTON GRADIENT AC MEMBRANE. THE GAMMA C TO BE IMPORTANT IN REGUL ACTIVITY AND THE FLOW O THROUGH THE CF(0) COMPL
CATALYTIC ACTIVITY	ATP + H(2)O + H(+)(IN) = ADP H(+)(OUT).
SUBUNIT	F-TYPE ATPASES HAVE 2 CO THE CATALYTIC CORE - ANI MEMBRANE PROTON CHAN SUBUNITS: ALPHA(3), BETA(DELTA(1), EPSILON(1). CF(0) SUBUNITS: A, B AND C.
SIMILARITY	BELONGS TO THE ATPASE G FAMILY.
CAUTION	REF.3 SEQUENCE DIFFERS FI DUE TO FRAMESHIFTS AND ERRORS.

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Database cross-references

	<u>X01631</u> ; <u>CAA25781.1</u> ; -.
	<u>J01594</u> ; <u>AAA24736.1</u> ; ALT_FRAME.
	<u>V00267</u> ; <u>CAA23526.1</u> ; -.
	<u>M25464</u> ; <u>AAA83874.1</u> ; -.



EMBL	<u>V00312</u> ; <u>CAA23597.1</u> ; ALT_FRAME. <u>L10328</u> ; <u>AAA62085.1</u> ; -. <u>AE000450</u> ; <u>AAC76756.1</u> ; -. <u>AE005605</u> ; <u>AAG58936.1</u> ; -. <u>AP002566</u> ; <u>BAB38098.1</u> ; -. <u>M34095</u> ; <u>AAA24742.1</u> ; -.
PIR	A01038; PWECEG. A01039; PWECEG2.
PDB	<u>1D8S</u> ; 03-DEC-99.
EcoGene	<u>EG10104</u> ; atpG.
InterPro	<u>IPR000131</u> ; ATPase_gamma.
Pfam	<u>PF00231</u> ; ATP-synt; 1.
PRINTS	<u>PR00126</u> ; ATPASEGAMMA.
TIGRFAMs	TIGR01146; ATPsyn_F1gamma; 1.
PROSITE	<u>PS00153</u> ; ATPASE_GAMMA; 1.

Keywords

ATP synthesis; CF(1); Hydrogen ion transport; Hydrolase; 3D-structure; Co

Sequence information

Length: **287 aa**, molecular weight: **31577 Da**, CRC64 checksum: **2417A4B8**

MAGAKEIRSK IASVQNTQKI TKAMEMVAAS KMRKSQDRMA ASRPYAETMR K
LEYKHPYLED RDVKRVGYLV VSTDRGLCGG LNINLFKKLL AEMKTWTDKG V
KGVSFNFNSVG GNVVAQVTGM GDNPSLSELI GPVKVMLQAY DEGRLDKLYI V
QVPTISQLLP LPASDDDDLK HKSWDYLYEP DPKALLDTLL RRYVESQVYQ G
AARMVAMKAA TDNGGSLIKE LQLVYNKARQ ASITQELTEI VSGAAAV
//

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IPB000131: ATP synthase gamma subunit

5 distinct blocks in 82 sequences

ATPG MYCGA	P33257	(289)	AAA---BBB-C-----DDD-EEEE
ATPG PROMO	P29710	(281)	AAA---BBB-C-----DDD-EEEE
ATPG RHORU	P07227	(299)	AAA---BBB-C-----DDD-EEEE
ATPG RICPR	O50289	(288)	AAA---BBB-C-----DDD-EEEE
ATPG ANASP	P12408	(315)	AAA---BBB-C-----DDD-EEEE
ATPG RHOBL	P05436	(286)	AAA---BBB-C-----DDD-EEEE
ATPG RHOCA	P72246	(290)	AAA---BBB-C-----DDD-EEEE
ATPG SPIPL	P50006	(310)	AAA---BBB-C-----DDD-EEEE
ATPG SYNPI	Q05384	(315)	AAA---BBB-C-----DDD-EEEE
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ATPG SYNPI	P17253	(314)	AAA---BBB-C-----DDD-EEEE
ATP1 ARATH	Q01908	(373)	-----AAA---BBB-C-----DDD-EEEE
ATP2 ARATH	Q01909	(386)	-----AAA---BBB-C-----DDD-EEEE-
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ATPG ODOSI	Q06908	(370)	-----AAA---BBB-C-----DDD-EEEE
ATPG PEA	P28552	(376)	-----AAA---BBB-C-----DDD-EEEE-
ATPG PHATR	Q41075	(370)	-----AAA---BBB-C-----DDD-EEEE
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ATPG TOBAC	P29790	(377)	-----AAA---BBB-C-----DDD-EEEE
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ATPG BACP3	P09222	(286)	-AAA---BBB-C-----DDD-EEEE
ATPG BUCAI	P57123	(290)	AAA---BBB-C-----DDD-EEEE-
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ATPG ECOLI	P00837	(287)	AAA---BBB-C-----DDD-EEEE
ATPG THIFE	P41169	(298)	AAA---BBB-C-----DDD-EEEE-
ATPG VIBAL	P12990	(288)	AAA---BBB-C-----DDD-EEEE
ATPG MYCGE	P47640	(279)	AAA---BBB-C-----DDD-EEEE
ATPG MYCPN	Q50330	(279)	AAA---BBB-C-----DDD-EEEE
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ATP3 IPOBA	P26360	(326)	-----AAA---BBB-C-----DDD-EEEE-
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ATPG HELPY	P56082	(301)	AAA---BBB-C-----DDD-EEEE
ATPG HELPJ	Q9ZK80	(301)	AAA---BBB-C-----DDD-EEEE
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Q9RQ80		(290)	AAA---BBB-C-----DDD-EEEE-

<u>Q9RQ77</u>	(290) <u>AAA</u> --- <u>BBB</u> -- <u>C</u> --- <u>DDD</u> --- <u>EEEE</u> -
<u>Q9RQ74</u>	(289) <u>AAA</u> --- <u>BBB</u> -- <u>C</u> --- <u>DDD</u> --- <u>EEEE</u> -
<u>Q9RGY2</u>	(320) <u>AAA</u> --- <u>BBB</u> -- <u>C</u> --- <u>DDD</u> --- <u>EEEE</u> -
<u>Q9RFL4</u>	(287) <u>AAA</u> --- <u>BBB</u> -- <u>C</u> --- <u>DDD</u> --- <u>EEEE</u> -
<u>Q9RAU1</u>	(289) <u>AAA</u> --- <u>BBB</u> -- <u>C</u> --- <u>DDD</u> --- <u>EEEE</u> -
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<u>Q9PJ20</u>	(294) <u>AAA</u> --- <u>BBB</u> -- <u>C</u> --- <u>DDD</u> --- <u>EEEE</u> -
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<u>Q9KNH4</u>	(288) <u>AAA</u> --- <u>BBB</u> -- <u>C</u> --- <u>DDD</u> --- <u>EEEE</u> -
<u>Q9K6H4</u>	(285) <u>AAA</u> --- <u>BBB</u> -- <u>C</u> --- <u>DDD</u> --- <u>EEEE</u> -
<u>Q9K4D4</u>	(305) <u>AAA</u> --- <u>BBB</u> -- <u>C</u> --- <u>DDD</u> --- <u>EEEE</u> -
<u>Q9JXQ1</u>	(291) <u>AAA</u> --- <u>BBB</u> -- <u>C</u> --- <u>DDD</u> --- <u>EEEE</u> -
<u>Q9JW71</u>	(291) <u>AAA</u> --- <u>BBB</u> -- <u>C</u> --- <u>DDD</u> --- <u>EEEE</u> -
<u>Q9HT19</u>	(286) <u>AAA</u> --- <u>BBB</u> -- <u>C</u> --- <u>DDD</u> --- <u>EEEE</u> -
<u>Q9FDR6</u>	(325) <u>AAA</u> --- <u>BBB</u> -- <u>C</u> --- <u>DDD</u> --- <u>EEEE</u> -
<u>Q9FAA4</u>	(325) <u>AAA</u> --- <u>BBB</u> -- <u>C</u> --- <u>DDD</u> --- <u>EEEE</u> -
<u>Q9CER9</u>	(289) <u>AAA</u> --- <u>BBB</u> -- <u>C</u> --- <u>DDD</u> --- <u>EEEE</u> -
<u>Q9ERA8</u>	(298) --- <u>AAA</u> --- <u>BBB</u> -- <u>C</u> --- <u>DDD</u> --- <u>EEEE</u> -
<u>Q9D9D7</u>	(298) --- <u>AAA</u> --- <u>BBB</u> -- <u>C</u> --- <u>DDD</u> --- <u>EEEE</u> -

---- 40 amino acids